AMENDMENTS TO THE CLAIMS

Please amend Claims 85, 87, 90, 92, 107, 109, 110-112, and 116-118 as shown below:

1-84. **(Cancelled)**

85. **(Currently amended)** A method for assessing the binding affinity between a candidate peptide and a target protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one peptide of known affinity for said target protein;

obtaining sequence data for said candidate peptide;

determining a first binding affinity for the candidate peptide for said target protein using a first predictive method, wherein said first predictive method employs the candidate peptide sequence data, and wherein said first predictive method is selected from the group consisting of quadratic programming, linear programming, anchor scoring, profile-based predictive methods, and structure-based predictive methods, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

determining a second binding affinity for the candidate peptide for said target protein using a second predictive method, wherein said second predictive method employs the candidate peptide sequence data, said second predictive method further comprising comparing the candidate peptide sequence data to the sequence data of the peptide of known affinity, wherein said second predictive method is selected from the group consisting of quadratic programming, linear programming, anchor scoring, profile-based predictive methods, and structure-based predictive methods, and wherein said second predictive method is different from the first predictive method, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

scaling said first binding affinity;

scaling said second binding affinity, said scaling of the first and second affinities comprising a method selected from the group consisting of 1) linearly scaling each binding affinity so that it has a value between 1 and 0, 2) nonlinearly scaling each binding affinity so that it has a value between 1 and 0, and 3) scaling the binding affinity in a

manner so a particular type of method can have a different weight, wherein a value is maintained between 1 and 0;

combining said first and second scaled binding affinities;

evaluating the combined first and second binding affinities as a basis for assessing a binding affinity between the candidate peptide and the target protein and

outputting the combined first and second scaled binding affinities to a user or a memory~~a result from the above steps~~.

86. **(Previously presented)** The method of Claim 85, wherein said target protein is a MHC class I protein and wherein said peptide comprises an epitope whereby said MHC class I protein binds to said peptide.

87. **(Currently amended)** The method of Claim 85, wherein said scaling comprises linearly scaling each binding affinity so that it has a value between 1 and 0.

88. **(Previously presented)** The method of Claim 85, wherein the candidate peptide is generated by dividing the sequence data of a known protein into ninemer or tenmer fragments.

89. **(Previously presented)** The method of Claim 85, wherein said first predictive method and said second predictive method are selected from the group consisting of quadratic programming, linear programming, anchor scoring, and profile-based scoring.

90. **(Currently amended)** A method for evaluating the binding affinity of a candidate peptide for a target protein, said method comprising:

obtaining for a plurality of known peptides, a collection of sequence and binding affinity information for said target protein;

obtaining sequence data for the candidate peptide;

predicting a first binding affinity for said candidate peptide for said target protein by evaluating the collection of sequence and binding affinity information for the plurality of known peptides, wherein the evaluation of the collection of sequence information comprises a comparison of the peptide sequences of the plurality of known peptides to the sequence data for the candidate peptide, wherein predicting is achieved by a method selected from the group consisting of quadratic programming, linear programming, profile-based, anchor scoring, and structure-based predictive methods, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

predicting a second binding affinity for said candidate peptide for said target protein by evaluating the collection of sequence and binding affinity information for the plurality of known peptides by a method that differs from the first binding affinity prediction, wherein predicting is achieved by a method selected from the group consisting of quadratic programming, linear programming, anchor scoring, profile-based and structure-based predictive methods, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

normalizing said first binding affinity to generate a first vote;

normalizing said second binding affinity to generate a second vote;

combining the first and second votes to obtain a score, wherein the score reflects the overall binding affinity of said candidate peptide for said target protein; and

outputting the score to a user or a memory~~a result from the above steps~~.

91. **(Previously presented)** The method of Claim 90, wherein said protein is a MHC class I protein and wherein said peptide comprises an epitope whereby the MHC class I protein binds to the peptide.

92. **(Currently amended)** The method of Claim 90, wherein said first and second binding affinity predictions are predicted by a method selected from the group comprising quadratic programming, linear programming, anchor scoring, and profile-based scoring, and wherein the second method is not the same method selected for the first method.

93-106. **(Cancelled)**

107. **(Currently amended)** A method for assessing the binding affinity between a candidate epitope and a MHC protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one epitope of known affinity for said MHC protein;

obtaining sequence data for said candidate epitope;

predicting a first binding affinity for the candidate epitope for said MHC protein using a first predictive method, wherein said prediction is a function of the candidate epitope sequence data, wherein said first prediction is performed on a computer, wherein the first binding affinity represents the likelihood that the candidate epitope will bind with the protein;

predicting a second binding affinity for the candidate epitope for said MHC protein by using a second predictive method, wherein said prediction comprises a comparison between the sequence data for the at least one epitope of known affinity and the sequence data for the candidate epitope in order to determine a similarity, and then using the similarity between the two sequences to predict the second binding affinity based upon the affinity of the peptide of known affinity, and wherein said second predictive method is different from said first predictive method, wherein said second prediction is performed on a computer, wherein the second binding affinity represents the likelihood that the candidate epitope will bind with the protein;

scaling the first and second predicted binding affinities before they are combined, said scaling comprising a method selected from the group consisting of 1) linearly scaling each binding affinity so that it has a value between 1 and 0, 2) nonlinearly scaling each binding affinity so that it has a value between 1 and 0, and 3) scaling the binding affinity in a manner so a particular type of method can have a different weight, wherein a value is maintained between 1 and 0;

combining said first and second scaled binding affinities;

evaluating the combined first and second binding affinities as a basis for assessing the binding affinity between the candidate epitope and the MHC protein; and

outputting the combined first and second scaled binding affinities to a user or a memory~~a result from the above steps~~.

108. **(Previously presented)** The method of Claim 107, wherein the MHC protein is a MHC class I protein.

109. **(Currently amended)** A method for assessing the binding affinity between a candidate peptide and a target protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one peptide of known affinity for said target protein;

obtaining sequence data for said candidate peptide;

determining a first binding affinity for the candidate peptide for said target protein using a first predictive method, wherein said determination employs the candidate peptide

sequence data to determine the first binding affinity, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

determining a second binding affinity for the candidate peptide for said target protein using a second predictive method, wherein said determination employs the candidate peptide sequence data to determine the second binding affinity, said second predictive method further comprising comparing the candidate peptide sequence data to the sequence data of the peptide of known affinity, and wherein said second predictive method is different from the first predictive method, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

scaling the first and second binding affinities, said scaling comprising linearly scaling each binding affinity so that it has a value between 1 and 0;

outputting said scaled first and second binding affinities to a user or a memory;

combining said first and second scaled binding affinities wherein the first and second binding affinities are scaled before they are combined; and

evaluating the combined first and second binding affinities as a basis for assessing the binding affinity between the candidate peptide and the target protein.

110. **(Currently amended)** A method for assessing the binding affinity between a candidate peptide and a target protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one peptide of known affinity for said target protein;

obtaining sequence data for said candidate peptide;

determining a first binding affinity for the candidate peptide for said target protein using a first predictive method, wherein said first predictive method employs the candidate peptide sequence data to determine the first binding affinity, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

determining a second binding affinity for the candidate peptide for said target protein using a second predictive method, wherein said second predictive method employs the candidate peptide sequence data to determine the second binding affinity, said second predictive method further comprises comparing the candidate peptide sequence data to the sequence data of the peptide of known affinity, and wherein said

second predictive method is different from the first predictive method, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

scaling the first and second binding affinities, said scaling comprising nonlinearly scaling each binding affinity so that it has a value between 1 and 0;

combining said first and second scaled binding affinities, wherein the first and second binding affinities are scaled before they are combined;

evaluating the combined first and second binding affinities as a basis for assessing the binding affinity between the candidate peptide and the target protein; and

outputting the evaluated combined first and second binding affinities to a user or a memory.

111. **(Currently amended)** A method for assessing the binding affinity between a candidate peptide and a target protein, said method comprising:

obtaining a collection of amino acid sequences and binding strength data for at least one peptide of known affinity for said target protein;

obtaining a sequence for said candidate peptide;

determining a first binding affinity for the candidate peptide for said target protein using a first predictive method, wherein said determination employs the candidate peptide sequence in order to determine the first binding affinity, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

determining a second binding affinity for the candidate peptide for said target protein using a second predictive method, wherein said determination employs the candidate peptide sequence in order to determine the second binding affinity, said second predictive method further comprises comparing the candidate peptide sequence to the sequence of the peptide of known affinity, and wherein said second predictive method is different from the first predictive method, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

scaling the first and second binding affinities in a manner so a particular type of predictive method can have a different weight, wherein a value is maintained between 1 and 0;

combining said first and second scaled binding affinities wherein the first and second binding affinities are scaled before they are combined;

evaluating the combined first and second binding affinities as a basis for assessing the binding affinity between the candidate peptide and the target protein; and

outputting the evaluation of the combined first and second binding affinities to a user or a memory~~at least one result from one of the above steps~~.

112. **(Currently amended)** A method for assessing the binding affinity between a candidate epitope and a MHC protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one epitope of known affinity for said MHC protein;

obtaining sequence data for said candidate epitope;

predicting a first binding affinity for the candidate epitope for said MHC protein using a first predictive method, wherein said prediction wherein predicting is achieved by at least one of the methods selected from the group consisting of quadratic programming, linear programming, profile-based and structure-based predictive methods, wherein said first prediction is performed on a computer, wherein the first binding affinity represents the likelihood that the candidate epitope will bind with the protein;

predicting a second binding affinity for the candidate epitope for said MHC protein by using a second predictive method, wherein predicting is achieved by at least one of the methods selected from the group consisting of a profile-based, quadratic programming, linear programming, and structure-based predictive methods, and wherein said second predictive method is different from said first predictive method, wherein said second prediction is performed on a computer, wherein the second binding affinity represents the likelihood that the candidate epitope will bind with the protein;

scaling the first and second predicted binding affinities before they are combined, said scaling comprising a method selected from the group consisting of 1) linearly scaling each binding affinity so that it has a value between 1 and 0, 2) nonlinearly scaling each binding affinity so that it has a value between 1 and 0, and 3) scaling the binding affinity in a manner so a particular type of method can have a different weight, wherein a value is maintained between 1 and 0;

combining said first and second binding affinities; and

outputting the combined first and second binding affinities to a user or a memory.

113. (**Previously presented**) The method of Claim 112, wherein the first predictive method is profile-based and the second predictive method is structure-based.

114. (**Previously presented**) The method of Claim 85, wherein the output is to a user.

115. (**Previously presented**) The method of Claim 85, wherein the output is to a memory.

116. (**Currently amended**) The method of Claim 112 wherein said first and second binding affinity are presented in terms selected from the group consisting of relative binding efficiencies, IC-50 values, and categorical binding affinities.

117. (**Currently amended**) The method of Claim 111 wherein said first and second binding affinity are presented in terms selected from the group consisting of relative binding efficiencies, IC-50 values, and categorical binding affinities..

118. (**Currently amended**) A method for assessing the binding affinity between a candidate peptide and a target protein, said method comprising:

obtaining a collection of sequence and binding strength data for at least one peptide of known affinity for said target protein;

obtaining sequence data for said candidate peptide;

determining a first binding affinity for the candidate peptide for said target protein using a first predictive method, wherein said first predictive method employs the candidate peptide sequence data, and wherein said first predictive method is selected from the group consisting of quadratic programming, linear programming, anchor scoring, profile-based predictive methods, and structure-based predictive methods, wherein the first binding affinity represents the likelihood that the peptide will bind with the protein;

determining a second binding affinity for the candidate peptide for said target protein using a second predictive method, wherein said second predictive method employs the candidate peptide sequence data, said second predictive method further comprising comparing the candidate peptide sequence data to the sequence data of the peptide of known affinity, wherein said second predictive method is selected from the

group consisting of quadratic programming, linear programming, anchor scoring, profile-based predictive methods, and structure-based predictive methods, and wherein said second predictive method is different from the first predictive method, wherein said first binding affinity and said second binding affinity are selected from the group consisting of relative binding efficiencies, IC-50 values, and categorical binding affinities, wherein the second binding affinity represents the likelihood that the peptide will bind with the protein;

scaling said first binding affinity;

scaling said second binding affinity, said scaling of the first and second affinities comprising a method selected from the group consisting of 1) linearly scaling each binding affinity so that it has a value between 1 and 0, 2) nonlinearly scaling each binding affinity so that it has a value between 1 and 0, and 3) scaling the binding affinity in a manner so a particular type of method can have a different weight, wherein a value is maintained between 1 and 0;

combining said first and second scaled binding affinities;

evaluating the combined first and second binding affinities as a basis for assessing a binding affinity between the candidate peptide and the target protein; and

outputting the combined first and second scaled binding affinities to a user or a memory~~a result from the above steps~~.